

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=2; day=17; hr=14; min=57; sec=40; ms=474; ]

=====

Application No: 10590526 Version No: 1.0

Input Set:

Output Set:

Started: 2009-01-30 15:06:14.257  
Finished: 2009-01-30 15:06:14.459  
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 202 ms  
Total Warnings: 2  
Total Errors: 0  
No. of SeqIDs Defined: 4  
Actual SeqID Count: 4

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)

# Sequence Listing

<110> Kodama, Tatsuhiko  
Hamakubo, Takao  
Ito, Yukio  
Iwanary, Hiroko  
Ohkuchi, Masao  
Sugiyama, Akira  
Perseus Proteomics Inc.

<120> Method for judging the extent of vasculopathy

<130> 295060US0PCT

<140> 10590526

<141> 2009-01-30

<150> JP 2004-049444

<151> 2004-02-25

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 1145

<212> DNA

<213> Homo sapiens

<400> 1

atgcatctcc ttgcgattct gttttgtgct ctctgggtctg cagtgttggc cgagaactcg	60
gatgattatg atctcatgta tgtgaatttg gacaacgaaa tagacaatgg actccatccc	120
actgaggacc ccacgcctg cgactgcggg caggagcact cggaatggga caagctcttc	180
atcatgctgg agaactcgca gatgagagag cgcattgctgc tgcaagccac ggacgacgtc	240
ctgcggggcg agctgcagag gctgcgggag gagctgggccc ggctcgcgga aagcctggcg	300
aggccgtgcg cgccggggggc tcccgcagag gccaggetga ccagtgtctt ggacgagctg	360
ctgcaggcga cccgcgacgc gggccgcagg ctggcgcgta tggagggcgc ggagggcgag	420
cgcccagagg agggggggcg cgccctggcc gcggtgctag aggagctgcg gcagacgcga	480
gccgacctgc acgcggtgca gggctgggct gcccgagct ggctgccggc aggttgtgaa	540
acagctatct tattcccaat gcgttccaag aagatctttg gaagcgtgca tccagtgaga	600
ccaatgaggc ttgagtcttt tagtgctctg atttggtgca aagccacaga tgtattaaac	660
aaaaccatcc tgttttctta tggcacaaaag aggaatccat atgaaatcca gctgtatctc	720
agctaccaat ccatagtgtt tgtgggtgggt ggagaggaga acaaactggt tgctgaagcc	780
atgggtttccc tgggaagggt gacccacctg tgcggcacct ggaattcaga ggaagggtc	840

```

acatccttgt gggtaaattg tgaactggcg gctaccactg ttgagatggc cacaggtcac      900
attgttcctg agggaggatc ctgcagattg gccaaagaaa gaatggctgc tgtgtgggtg      960
gtggctttga tgaacatta gccttctctg ggagactcac aggcttcaat atctgggata     1020
gtgttcttag caatgaagag ataagagaga ccggaggagc agagtcttgt cacatccggg     1080
ggaatattgt tgggtgggga gtcacagaga tccagccaca tggaggagct cagtatgttt     1140
cataa                                           1145

```

```

<210>  2
<211> 381
<212>  PRT
<213>  Homo sapiens

<400>  2

```

```

Met His Leu Leu Ala Ile Leu Phe Cys Ala Leu Trp Ser Ala Val Leu
1              5              10              15

```

```

Ala Glu Asn Ser Asp Asp Tyr Asp Leu Met Tyr Val Asn Leu Asp Asn
              20              25              30

```

```

Glu Ile Asp Asn Gly Leu His Pro Thr Glu Asp Pro Thr Pro Cys Asp
35              40              45

```

```

Cys Gly Gln Glu His Ser Glu Trp Asp Lys Leu Phe Ile Met Leu Glu
50              55              60

```

```

Asn Ser Gln Met Arg Glu Arg Met Leu Leu Gln Ala Thr Asp Asp Val
65              70              75              80

```

```

Leu Arg Gly Glu Leu Gln Arg Leu Arg Glu Glu Leu Gly Arg Leu Ala
              85              90              95

```

```

Glu Ser Leu Ala Arg Pro Cys Ala Pro Gly Ala Pro Ala Glu Ala Arg
100              105              110

```

```

Leu Thr Ser Ala Leu Asp Glu Leu Leu Gln Ala Thr Arg Asp Ala Gly
115              120              125

```

```

Arg Arg Leu Ala Arg Met Glu Gly Ala Glu Ala Gln Arg Pro Glu Glu
130              135              140

```

Ala Gly Arg Ala Leu Ala Ala Val Leu Glu Glu Leu Arg Gln Thr Arg  
145 150 155 160

Ala Asp Leu His Ala Val Gln Gly Trp Ala Ala Arg Ser Trp Leu Pro  
165 170 175

Ala Gly Cys Glu Thr Ala Ile Leu Phe Pro Met Arg Ser Lys Lys Ile  
180 185 190

Phe Gly Ser Val His Pro Val Arg Pro Met Arg Leu Glu Ser Phe Ser  
195 200 205

Ala Cys Ile Trp Val Lys Ala Thr Asp Val Leu Asn Lys Thr Ile Leu  
210 215 220

Phe Ser Tyr Gly Thr Lys Arg Asn Pro Tyr Glu Ile Gln Leu Tyr Leu  
225 230 235 240

Ser Tyr Gln Ser Ile Val Phe Val Val Gly Gly Glu Glu Asn Lys Leu  
245 250 255

Val Ala Glu Ala Met Val Ser Leu Gly Arg Trp Thr His Leu Cys Gly  
260 265 270

Thr Trp Asn Ser Glu Glu Gly Leu Thr Ser Leu Trp Val Asn Gly Glu  
275 280 285

Leu Ala Ala Thr Thr Val Glu Met Ala Thr Gly His Ile Val Pro Glu  
290 295 300

Gly Gly Ile Leu Gln Ile Gly Gln Glu Lys Asn Gly Cys Cys Val Gly  
305 310 315 320

Gly Gly Phe Asp Glu Thr Leu Ala Phe Ser Gly Arg Leu Thr Gly Phe  
325 330 335

Asn Ile Trp Asp Ser Val Leu Ser Asn Glu Glu Ile Arg Glu Thr Gly  
340 345 350

Gly Ala Glu Ser Cys His Ile Arg Gly Asn Ile Val Gly Trp Gly Val  
355 360 365

Thr Glu Ile Gln Pro His Gly Gly Ala Gln Tyr Val Ser

370

375

380

<210> 3

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence for amplification of NM\_002852

<400> 3

cggggtatgc atctccttgc gattctgttt

30

<210> 4

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence for amplification of NM\_002852

<400> 4

cgcggatcct tatgaaacat actgagctcc tccatgtg

38